



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Suerbaum, Sebastian
Labigne, Agnes
- (ii) TITLE OF INVENTION: Cloning and Characterization of the flbA
Gene of H. Pylori, Production of Aflagellate Strains
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner
 - (B) STREET: 1300 I Street, N.W.
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3315
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/671,757
 - (B) FILING DATE: 28-JUN-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Meyers, Kenneth J.
 - (B) REGISTRATION NUMBER: 25,146
 - (C) REFERENCE/DOCKET NUMBER: 02356.0073-00000
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 408-4000
 - (B) TELEFAX: (202) 408-4400

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGCCTCGAG GTCGAAAAGC AAGATG

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAAATCTTCA TACTGGCAGC TCCAGTC

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGCCAGGAA AGCAAATGGC GATTGATGCG GATTTAAATT CAGGGCTTAT TGATGATAAG	60
GAAGCTAAAA AACGGCGCGC CGCTCTAACGC CAAGAAGCGG ATTTTATGG TGCGATGGAT	120
GGCGCGTCTA AATTT	135

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGGATCCGT GGTTACTAAT GGTTCTAC

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGGATCCTC ATGGCCTCTT CAGAGACC

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCTTTTTG TGCCATACTT TTAAACTTTA TATTATAATA AGAGACAAAC ACACCTACCA	60
AAATTAAGGC ATTGATTAA GATTATGGCA AACGAACGCT CCAAATTAGC TTTTAAAAAG	120
ACTTTCCCTG TCTTAAACG CTTCTGCAA TCCAAAGACT TAGCCCTTGT GGTCTTTGTG	180
ATAGCGATTT TAGCGATCAT TATCGTGCCG TTACCGCCTT TTGTGTTGGA TTTTTTACTC	240
ACGATTCTA TCGCGCTATC GGTGTTGATT ATTTTAATCG GGCTTTATAT TGACAAACCG	300
ACTGATTTA GCGCTTCCC CACTTTATTA CTCATTGTAA CCTTATACCG CTTGGCTTTA	360
AATGTCGCCA CCACTAGAAT GATTTAACCC CAAGGCTATA AAGGGCCTAG CGCGGTGAGC	420
ATTATTATCA CGGCGTTGGG GGAATTAGC GTGAGCGGGGA ATTATGTGAT TGGGGCTATT	480
ATCTTAGTA TTTTAGTGCT GGTGAATTAA TTAGTGGTTA CTAATGGTC TACTAGGGTT	540
ACTGAAGTTA GGGCGCGATT TGCCCTAGAC GCTATGCCAG GAAAGCAAAT GGCGATTGAT	600
CGGGATTAA ATTCAAGGGCT TATTGATGAT AAGGAAGCTA AAAAACGGCG CGCCGCTCTA	660
AGCCAAGAAG CGGATTTTA TGGTGCGATG GATGGCGCGT CTAAATTGT CAAAGGCGAT	720
GCGATCGCTT CTATCATTAT CACGCTTATC AATATCATTG GGGGTTTTT AGTGGCGTG	780
TTCCAAAGGG ATATGAGCTT GAGCTTAGT GCTAGCACCT TCACATCTT AACCAATTGGC	840
GATGGGCTTG TAGGGCAAAT CCCTGCCTTA ATCATTGCGA CACGGACCGG TATTGTCGCC	900
ACTCGCACCA CGCAAAACGA AGAAGAGGAC TTTGCTTCTA AGCTCATCAC ACAGCTCACC	960
AATAAAAGCA AAACTTAGT GATTGTGGGG GCGATTTATT GCTTTGCAC CATTCCCTGGA	1020

CTCCCTACCT TTTCTTTAGC GTTTGTAGGG GCTCTCTTT TATTCATCGC ATGGCTGATT	1080
AGCAGGGAGG GAAAGGACGG GTTGCTCACT AAATTAGAAA ATTATTTGAG TCAAAAATTC	1140
GGCTTGGATT TGAGCGAAAA ACCCCACAGC TCCAAAATCA AACCCCACGC CCCCACCACA	1200
AGGGCTAAAA CCCAAGAAGA GATTAAAAGA GAAGAAGAGC AAGCCATTGA TGAAGTGTAA	1260
AAAATTGAAT TTTTAGAATT GGCTTTAGGC TATCAGCTCT ACAGCTTAGC GGACATGAAA	1320
CAAGGGGGCG ATTGTGTTAGA AAGGATTAGG GGTATTAGAA AAAAGATAGC GAGCGATTAT	1380
GGTTTTTGA TGCCTCAAAT TAGGATTAGG GATAATTAC AACTCCCCC AACGCATTAT	1440
GAAATCAAGC TTAAGGGCAT TGTGATTGGT GAAGGCATGG TGATGCCGGA TAAGTTTTA	1500
GCCATGAATA CCGGTTTTGT GAATAAAGAA ATTGAAGGCA TTCTACTAA AGAGCCGGCT	1560
TTTCCAATGG ACGCTTTATG GATTGAAACT AAAAATAAAG AAGAAGCCAT CATTCAAGGC	1620
TATACCATTA TTGATCCAAG CACCGTTATT GCGACGCACA CCAGCGAATT AGTAAAAAAA	1680
TACGCTGAAG ATTTTATCAC TAAAGATGAA GTGAAATCCC TTTAGAGCG CTTGGCCAAA	1740
GACTATCCTA CGATTGTAGA AGAGAGTAAA AAAATCCCC CCGGTGCGAT CCGATCAGTC	1800
TTGCAAGCCT TGTTGCATGA AAAAATCCCC ATTAAAGACA TGCTCACTAT TTTAGAAACG	1860
ATTACCGATA TTGCGCCATT AGTTCAAAAC GATGTGAATA TCTTAACCGA ACAAGTGAGG	1920
GCGAGGCTTT CTAGGGTGAT CACTAACGCT TTTAAATCTG AAGACGGGCG TTTGAAATTT	1980
TTAACCTTT CTACCGATAG CGAACAAATT TTGCTTAATA AATTGCGAGA AAATGGCACT	2040
TCTAAGAGCC TACTACTCAA TGTGGCGAA TTGCAAAAC TCATTGAAGC GGTCTCTGAA	2100
GAGGCCATGA AAGTCTTGCA AAAAGGGATC GCTCCGGTGA TTTGATCGT AGAGCCTAAT	2160
TTAAGAAAAG CCCTTTCTAA TCAAATGGAG CAGGCTAGGA TTGATGTAAT CGTGCTAAGC	2220
CATGCTGAAT TAGATCCTAA CTCTAATTTT GAAGCCTTAG GCACGATCCA TATTAACCTT	2280
TAAGGGATAA ATAATTGATA AAAAAGGAGA ATGATGCAAG TTTATCACCT TTCACACATT	2340
GATTTAGACG GCTATGCATG CCAGCTTGTT TCAAAACAAT TTTTAAAAAA TATCCAATGC	2400
TATAACGCTA ATTACGGGCG TGAAGTCTCA GCGAGAATT ATGAGATTT AAACGCGATC	2460
GCTCAATCTA AAGAGAGTGA ATTCTTATT TTGATTAGCG A	2501

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ala	Asn	Glu	Arg	Ser	Lys	Leu	Ala	Phe	Lys	Lys	Thr	Phe	Pro	Val
1															15
Phe Lys Arg Phe Leu Gln Ser Lys Asp Leu Ala Leu Val Val Phe Val															
									20	25				30	
Ile	Ala	Ile	Leu	Ala	Ile	Ile	Ile	Val	Pro	Leu	Pro	Pro	Phe	Val	Leu
									35	40				45	
Asp	Phe	Leu	Leu	Thr	Ile	Ser	Ile	Ala	Leu	Ser	Val	Leu	Ile	Ile	Leu
									50	55				60	
Ile	Gly	Leu	Tyr	Ile	Asp	Lys	Pro	Thr	Asp	Phe	Ser	Ala	Phe	Pro	Thr
									65	70				80	
Leu	Leu	Leu	Ile	Val	Thr	Leu	Tyr	Arg	Leu	Ala	Leu	Asn	Val	Ala	Thr
									85		90			95	
Thr	Arg	Met	Ile	Leu	Thr	Gln	Gly	Tyr	Lys	Gly	Pro	Ser	Ala	Val	Ser
									100	105				110	
Ile	Ile	Ile	Thr	Ala	Phe	Gly	Glu	Phe	Ser	Val	Ser	Gly	Asn	Tyr	Val
									115	120				125	
Ile	Gly	Ala	Ile	Ile	Phe	Ser	Ile	Leu	Val	Leu	Val	Asn	Leu	Leu	Val
									130	135				140	
Val	Thr	Asn	Gly	Ser	Thr	Arg	Val	Thr	Glu	Val	Arg	Ala	Arg	Phe	Ala
									145	150				155	
Leu	Asp	Ala	Met	Pro	Gly	Lys	Gln	Met	Ala	Ile	Asp	Ala	Asp	Leu	Asn
									165		170			175	

Ser Gly Leu Ile Asp Asp Lys Glu Ala Lys Lys Arg Arg Ala Ala Leu
180 185 190

Ser Gln Glu Ala Asp Phe Tyr Gly Ala Met Asp Gly Ala Ser Lys Phe
195 200 205

Val Lys Gly Asp Ala Ile Ala Ser Ile Ile Ile Thr Leu Ile Asn Ile
210 215 220

Ile Gly Gly Phe Leu Val Gly Val Phe Gln Arg Asp Met Ser Leu Ser
225 230 235 240

Phe Ser Ala Ser Thr Phe Thr Ile Leu Thr Ile Gly Ala Gly Leu Val
245 250 255

Gly Gln Ile Pro Ala Leu Ile Ile Ala Thr Arg Thr Gly Ile Val Ala
260 265 270

Thr Arg Thr Thr Gln Asn Glu Glu Asp Phe Ala Ser Lys Leu Ile
275 280 285

Thr Gln Leu Thr Asn Lys Ser Lys Thr Leu Val Ile Val Gly Ala Ile
290 295 300

Tyr Cys Phe Cys Thr Ile Pro Gly Leu Pro Thr Phe Ser Leu Ala Phe
305 310 315 320

Val Gly Ala Leu Phe Leu Phe Ile Ala Trp Leu Ile Ser Arg Glu Gly
325 330 335

Lys Asp Gly Leu Leu Thr Lys Leu Glu Asn Tyr Leu Ser Gln Lys Phe
340 345 350

Gly Leu Asp Leu Ser Glu Lys Pro His Ser Ser Lys Ile Lys Pro His
355 360 365

Ala Pro Thr Thr Arg Ala Lys Thr Gln Glu Glu Ile Lys Arg Glu Glu
370 375 380

Glu Gln Ala Ile Asp Glu Val Leu Lys Ile Glu Phe Leu Glu Leu Ala
385 390 395 400

Leu Gly Thr Gln Leu Tyr Ser Leu Ala Asp Met Lys Gln Gly Gly Asp
405 410 415

Leu Leu Glu Arg Ile Arg Gly Ile Arg Lys Lys Ile Ala Ser Asp Tyr
420 425 430

Gly Phe Leu Met Pro Gln Ile Arg Ile Arg Asp Asn Leu Gln Leu Pro
435 440 445

Pro Thr His Tyr Glu Ile Lys Leu Lys Gly Ile Val Ile Gly Glu Gly
450 455 460

Met Val Met Pro Asp Lys Phe Leu Ala Met Asn Thr Gly Phe Val Asn
465 470 475 480

Lys Glu Ile Glu Gly Ile Pro Thr Lys Glu Pro Ala Phe Gly Met Asp
485 490 495

Ala Leu Trp Ile Glu Thr Lys Asn Lys Glu Glu Ala Ile Ile Gln Gly
500 505 510

Tyr Thr Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser Glu
515 520 525

Leu Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys
530 535 540

Ser Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu
545 550 555 560

Ser Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu
565 570 575

Leu His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr
580 585 590

Ile Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr
595 600 605

Glu Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys
610 615 620

Ser Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Ser Glu
625 630 635 640

Gln Phe Leu Leu Asn Lys Leu Arg Glu Asn Gly Thr Ser Lys Ser Leu
645 650 655

Leu Leu Asn Val Gly Glu Leu Gln Lys Leu Ile Glu Ala Val Ser Glu
660 665 670

Glu Ala Met Lys Val Leu Gln Lys Gly Ile Ala Pro Val Ile Leu Ile
675 680 685

Val Glu Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln Ala
690 695 700

Arg Ile Asp Val Ile Val Leu Ser His Ala Glu Leu Asp Pro Asn Ser
705 710 715 720

Asn Phe Glu Ala Leu Gly Thr Ile His Ile Asn Phe
725 730

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ala	Asn	Glu	Arg	Ser	Lys	Leu	Ala	Phe	Lys	Lys	Thr	Phe	Pro	Val	
1					5									10		15
Phe Lys Arg Phe Leu Gln Ser Lys Asp Leu Ala Leu Val Val Phe Val																
					20					25				30		
Ile	Ala	Ile	Leu	Ala	Ile	Ile	Ile	Val	Pro	Leu	Pro	Pro	Phe	Val	Leu	
					35					40				45		
Asp	Phe	Leu	Leu	Thr	Ile	Ser	Ile	Ala	Leu	Ser	Val	Leu	Ile	Ile	Leu	
					50				55			60				
Ile	Gly	Leu	Tyr	Ile	Asp	Lys	Pro	Thr	Asp	Phe	Ser	Ala	Phe	Pro	Thr	
					65			70		75			80			
Leu	Leu	Leu	Ile	Val	Thr	Leu	Tyr	Arg	Leu	Ala	Leu	Asn	Val	Ala	Thr	
					85				90				95			
Thr	Arg	Met	Ile	Leu	Thr	Gln	Gly	Tyr	Lys	Gly	Pro	Ser	Ala	Val	Ser	
					100				105				110			
Ile	Ile	Ile	Thr	Ala	Phe	Gly	Glu	Phe	Ser	Val	Ser	Gly	Asn	Tyr	Val	
					115				120			125				
Ile	Gly	Ala	Ile	Ile	Phe	Ser	Ile	Leu	Val	Leu	Val	Asn	Leu	Leu	Val	
					130			135			140					
Val	Thr	Asn	Gly	Ser	Thr	Arg	Val	Thr	Glu	Val	Arg	Ala	Arg	Phe	Ala	
					145				150		155			160		
Leu	Asp	Ala	Met	Pro	Gly	Lys	Gln	Met	Ala	Ile	Asp	Ala	Asp	Leu	Asn	
					165				170				175			

Ser Gly Leu Ile Asp Asp Lys Glu Ala Lys Lys Arg Arg Ala Ala Leu
180 185 190

Ser Gln Glu Ala Asp Phe Tyr Gly Ala Met Asp Gly Ala Ser Lys Phe
195 200 205

Val Lys Gly Asp Ala Ile Ala Ser Ile Ile Ile Thr Leu Ile Asn Ile
210 215 220

Ile Gly Gly Phe Leu Val Gly Val Phe Gln Arg Asp Met Ser Leu Ser
225 230 235 240

Phe Ser Ala Ser Thr Phe Thr Ile Leu Thr Ile Gly Asp Gly Leu Val
245 250 255

Gly Gln Ile Pro Ala Leu Ile Ile Ala Thr Arg Thr Gly Ile Val Ala
260 265 270

Thr Arg Thr Thr Gln Asn Glu Glu Asp Phe Ala Ser Lys Leu Ile
275 280 285

Thr Gln Leu Thr Asn Lys Ser Lys Thr Leu Val Ile Val Gly Ala Ile
290 295 300

Tyr Cys Phe Cys Thr Ile Pro Gly Leu Pro Thr Phe Ser Leu Ala Phe
305 310 315 320

Val Gly Ala Leu Phe Leu Phe Ile Ala Trp Leu Ile Ser Arg Glu Gly
325 330 335

Lys Asp Gly Leu Leu Thr Lys Leu Glu Asn Tyr Leu Ser Gln Lys Phe
340 345 350

Gly Leu Asp Leu Ser Glu Lys Pro His Ser Ser Lys Ile Lys Pro His
355 360 365

Ala Pro Thr Thr Arg Ala Lys Thr Gln Glu Glu Ile Lys Arg Glu Glu
370 375 380

Glu Gln Ala Ile Asp Glu Val Leu Lys Ile Glu Phe Leu Glu Leu Ala
385 390 395 400

Leu Gly Tyr Gln Leu Tyr Ser Leu Ala Asp Met Lys Gln Gly Gly Asp
405 410 415

Leu Leu Glu Arg Ile Arg Gly Ile Arg Lys Lys Ile Ala Ser Asp Tyr
420 425 430

Gly Phe Leu Met Pro Gln Ile Arg Ile Arg Asp Asn Leu Gln Leu Pro
435 440 445

Pro Thr His Tyr Glu Ile Lys Leu Lys Gly Ile Val Ile Gly Glu Gly
450 455 460

Met Val Met Pro Asp Lys Phe Leu Ala Met Asn Thr Gly Phe Val Asn
465 470 475 480

Lys Glu Ile Glu Gly Ile Pro Thr Lys Glu Pro Ala Phe Gly Met Asp
485 490 495

Ala Leu Trp Ile Glu Thr Lys Asn Lys Glu Glu Ala Ile Ile Gln Gly
500 505 510

Tyr Thr Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser Glu
515 520 525

Leu Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys
530 535 540

Ser Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu
545 550 555 560

Ser Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu
565 570 575

Leu His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr
580 585 590

Ile Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr
595 600 605

Glu Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys
610 615 620

Ser Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Ser Glu
625 630 635 640

Gln Phe Leu Leu Asn Lys Leu Arg Glu Asn Gly Thr Ser Lys Ser Leu
645 650 655

Leu Leu Asn Val Gly Glu Leu Gln Lys Leu Ile Glu Ala Val Ser Glu
660 665 670

Glu Ala Met Lys Val Leu Gln Lys Gly Ile Ala Pro Val Ile Leu Ile
675 680 685

Val Glu Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln Ala
690 695 700

Arg Ile Asp Val Ile Val Leu Ser His Ala Glu Leu Asp Pro Asn Ser
705 710 715 720

Asn Phe Glu Ala Leu Gly Thr Ile His Ile Asn Phe
725 730

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Lys Asn Lys Ile Val Asp Leu Val Phe Pro Phe Leu Gly Pro
1 5 10 15

Leu Ile Ala Pro Val Leu Lys Ala Lys Ser Leu Thr Ile Val Gly Phe
20 25 30

Leu Val Cys Ile Leu Ala Ile Ile Val Pro Leu Pro Ser Pro Ile
35 40 45

Leu Asp Phe Phe Leu Ala Leu Ser Ile Ala Leu Ser Val Leu Ile Ile
50 55 60

Leu Ile Ser Ile Tyr Ile Pro Lys Pro Thr Asp Leu Thr Thr Phe Pro
65 70 75 80

Thr Leu Ile Leu Ile Ile Thr Leu Phe Arg Leu Ser Leu Asn Ile Ala
85 90 95

Thr Thr Arg Met Ile Leu Ser Glu Gly Gln Asn Gly Pro Glu Ala Val
100 105 110

Ser Glu Ile Ile Ala Ala Phe Gly Glu Phe Val Val Gly Gly Asn Met
115 120 125

Val Ile Gly Val Ile Val Phe Cys Ile Leu Val Leu Ile Asn Phe Met
130 135 140

Val Val Thr Lys Gly Ser Thr Arg Val Ser Glu Val Gln Ala Arg Phe
145 150 155 160

Thr Leu Asp Ala Met Pro Gly Lys Gln Met Ala Ile Asp Ala Asp Leu
165 170 175

Asn Ala Gly Leu Ile Asp Glu Gln Thr Ala Arg Ala Arg Arg Gln Glu
180 185 190

Val Ile Ala Glu Ala Asn Phe Tyr Gly Ala Met Asp Gly Ser Ser Lys
195 200 205

Phe Ile Lys Gly Asp Ala Val Ala Gly Ile Ile Ile Thr Ile Ile Asn
210 215 220

Ile Ile Gly Gly Phe Leu Ile Gly Ser Phe Gln His Asp Met Ala Leu
225 230 235 240

Ser Asp Ala Ala Ser Thr Tyr Thr Ile Leu Thr Ile Gly Asp Gly Leu
245 250 255

Val Ser Gln Ile Pro Gly Leu Ile Thr Ser Thr Ala Thr Ala Ile Ile
260 265 270

Ile Thr Arg Ala Ser Lys Asp Glu Glu Asn Phe Ala Glu Gly Thr Leu
275 280 285

Thr Gln Leu Leu Ser Glu Tyr Arg Thr Leu Leu Ile Val Gly Phe Val
290 295 300

Leu Phe Ile Phe Ala Leu Val Pro Gly Leu Pro Thr Leu Ser Leu Gly
305 310 315 320

Phe Met Ala Leu Val Phe Leu Ser Leu Gly Tyr Leu Tyr Lys Gln Val
325 330 335

Lys Glu Gly Lys Ile Asp Ile Thr Thr Val Lys Lys Ser Lys Pro Ser
340 345 350

Ala Ala Val Ala Ser Gln Ser Gly Ala Gly Gly Thr Thr Ala Ala Pro
355 360 365

Ala Lys Lys Ser Glu Glu Glu Ile Leu Lys Glu Glu Glu His Lys Ile
370 375 380

Asn Asp Ile Leu Lys Val Glu Ile Leu Glu Leu Glu Leu Gly Tyr Gly
385 390 395 400

Leu Ile Lys Leu Ala Glu Asn Glu Leu Thr Glu Arg Ile Arg Ser Met
405 410 415

Arg Arg Ser Ile Ala Glu Ser Leu Gly Phe Leu Met Pro Lys Ile Arg
420 425 430

Ile Arg Asp Asn Leu Arg Leu Lys Pro Asn Glu Tyr Ser Phe Lys Leu
435 440 445

Lys Gly Val Ser Ile Ala Ser Ala Glu Ile Tyr Pro Asp Lys Tyr Leu
450 455 460

Ala Met Asp Ser Gly Phe Ile Thr Glu Glu Ile Glu Gly Ile Ala Thr
465 470 475 480

Lys Glu Pro Ala Phe Asn Ser Asp Ala Leu Trp Ile Asp Ala Asn Leu
485 490 495

Lys Asp Glu Ala Thr Leu Asn Gly Tyr Ile Val Ile Asp Pro Ala Ser
500 505 510

Val Ile Ser Thr His Met Ser Glu Leu Ala Lys Ala His Ala Ser Glu
515 520 525

Leu Leu Thr Arg Gln Glu Val Gln Asn Leu Leu Asp Lys Val Lys Asn
530 535 540

Asp Tyr Pro Ile Ile Val Glu Gly Ala Leu Gly Val Ala Pro Val Ser
545 550 555 560

Leu Ile Gln Lys Ile Leu Lys Asp Leu Leu Lys His His Ile Pro Ile
565 570 575

Lys Asp Met Leu Thr Ile Leu Glu Ser Val Ser Asp Ile Ala Glu Val
580 585 590

Ser Lys Ser Phe Asp Met Ile Ile Glu His Val Arg Ala Ser Leu Ala
595 600 605

Arg Met Ile Thr Asn Met Tyr Leu Asp Asp Lys Gly Asn Leu Asp Ile
610 615 620

Phe Ile Leu Asp Ser Ala Ser Ser Ala Val Leu Met Glu Asn Val Gln
625 630 635 640

Phe Arg Asp Gly Ser Tyr His Leu Pro Leu Ser Val Ala Gln Thr Gly
645 650 655

Thr Leu Val Asp Thr Leu Arg Ala Glu Val Ala Ala Val Ala Asn Gly
660 665 670

Arg Ile Lys Pro Phe Ile Leu Cys Val Glu Pro Gln Leu Arg Lys Phe
675 680 685

Ile Ala Asp Ile Cys Tyr Asn Phe Ser Ile Asn Ile Val Val Leu Ser
690 695 700

Phe Ala Glu Ile Ala Glu Asn Thr Asn Phe Asn Thr Glu Gly Ile Ile
705 710 715 720

Arg Ile Glu Leu

(2) INFORMATION FOR SEO ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Asp Ala Ala Ala Pro Asn Ala Ser Ser Met Pro Ser Ala Lys
1 5 10 15

Ser Leu Leu Asp Gly Leu Met Arg Gly Glu Met Gly Leu Ala Leu Gly
20 25 30

Val Val Gly Ile Ile Val Leu Leu Ile Ile Pro Val Pro Ala Pro Leu
 35 40 45

Leu Asp Val Leu Leu Ala Ile Ser Leu Thr Gly Ser Val Leu Ile Leu
50 55 60

Met Thr Ala Ile Leu Ile Lys Lys Pro Leu Glu Phe Thr Ser Phe Pro
65 70 75 80

Thr Val Leu Leu Val Thr Thr Leu Phe Arg Leu Gly Leu Asn Ile Ala
85 90 95

Ser Thr Arg Leu Ile Leu Ser His Gly Gln Glu Gly Thr Gly Gly Ala
100 105 110

Gly Ala Val Ile Glu Ala Phe Gly His Leu Met Met Gln Gly Asn Phe
115 120 125

Val Ile Gly Val Ile Val Phe Ile Ile Leu Ile Val Val Asn Phe Met
130 135 140

Val Val Thr Lys Gly Ser Gly Arg Ile Ala Glu Val Ala Ala Arg Phe
145 150 155 160

Thr Leu Asp Ser Met Pro Gly Lys Gln Met Ala Ile Asp Ala Asp Leu
165 170 175

Ser Thr Gly Leu Ile Ser Gln Asp Glu Ala Lys Ile Arg Arg Lys Glu
180 185 190

Leu Glu Gln Glu Ser Thr Phe Phe Gly Ala Met Asp Gly Ala Ser Lys
195 200 205

Phe Val Lys Gly Asp Ala Ile Ala Gly Leu Ile Ile Thr Ala Ile Asn
210 215 220

Ile Ile Gly Gly Ile Ile Gly Val Val Gln His Lys Met Pro Phe
225 230 235 240

Gly Asp Ala Ala Ser Thr Tyr Thr Ile Met Thr Ile Gly Asp Gly Leu
245 250 255

Val Ser Gln Ile Pro Ala Leu Ile Ile Ser Ile Ala Ala Gly Met Val
260 265 270

Val Ser Lys Ala Gly Val Glu Gly Ser Ala Asp Lys Ala Leu Thr Thr
275 280 285

Gln Leu Ala Met Asn Pro Val Gly Leu Gly Met Val Ser Ala Ser Ser
290 295 300

Gly Ile Ile Ala Leu Ile Pro Gly Met Pro Ile Phe Pro Phe Ala Ala
305 310 315 320

Met Ala Leu Ala Ala Gly Ala Leu Ala Tyr Lys Arg Val Gln Asp Ala
325 330 335

Lys Lys Pro Lys Ala Leu Asp Pro Ala Asp Leu Glu Ala Ala Ala Pro
340 345 350

Ser Glu Pro Glu Glu Glu Pro Ile Ser Ala Ser Leu Ala Ile Asp Asp
355 360 365

Val Lys Ile Glu Leu Gly Tyr Gly Leu Leu Thr Leu Ile Asn Asp Leu
370 375 380

Asp Gly Arg Lys Leu Thr Asp Gln Ile Arg Ala Leu Arg Lys Thr Leu
385 390 395 400

Ala Ser Glu Tyr Gly Phe Val Met Pro Pro Val Arg Ile Leu Asp Asn
405 410 415

Met Arg Leu Ala Asn Gln Gly Tyr Ala Ile Arg Ile Lys Glu Met Glu
420 425 430

Ala Gly Ala Gly Glu Val Arg Leu Gly Cys Leu Met Cys Met Asp Pro
435 440 445

Arg Gly Gly Gln Val Glu Leu Pro Gly Glu His Val Arg Glu Pro Ala
450 455 460

Phe Gly Leu Pro Ala Thr Trp Ile Ala Asp Asp Leu Arg Glu Glu Ala
465 470 475 480

Thr Phe Arg Gly Tyr Thr Val Val Asp Pro Ala Thr Val Leu Thr Thr
485 490 495

His Leu Thr Glu Ile Leu Lys Glu Asn Met Ala Asp Leu Leu Ser Tyr
500 505 510

Ala Glu Val Gln Lys Leu Leu Lys Glu Leu Pro Glu Thr Gln Lys Lys
515 520 525

Leu Val Asp Asp Leu Ile Pro Gly Thr Val Thr Ala Thr Thr Val Gln
530 535 540

Arg Val Leu Gln Ser Leu Leu Arg Glu Arg Val Ser Ile Arg Asp Leu
545 550 555 560

Pro Gln Ile Leu Glu Gly Val Gly Glu Ala Ala Pro His Thr Ala Ser
565 570 575

Val Thr Gln Leu Val Glu Gln Val Arg Ala Arg Leu Ala Arg Gln Leu
580 585 590

Cys Trp Ala Asn Arg Gly Asp Asp Gly Ala Leu Pro Ile Ile Thr Leu
595 600 605

Ser Ala Asp Trp Glu Gln Ala Phe Ala Glu Ala Leu Ile Gly Pro Gly
610 615 620

Asp Asp Lys Gln Leu Ala Leu Pro Pro Ser Arg Leu Gln Asp Phe Ile
625 630 635 640

Arg Gly Val Arg Asp Ser Phe Glu Arg Ala Ala Leu Ala Gly Glu Ala
645 650 655

Pro Val Leu Leu Thr Ser Pro Gly Val Arg Pro Tyr Val Arg Ser Ile
660 665 670

Ile Glu Arg Phe Arg Gly Gln Thr Val Val Met Ser Gln Asn Glu Ile
675 680 685

His Pro Arg Ala Arg Leu Lys Thr Val Gly Met Val
690 695 700

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Asn	Pro	His	Asp	Leu	Glu	Trp	Leu	Asn	Arg	Ile	Gly	Glu	Arg	Lys
1				5					10					15	
Asp	Ile	Met	Leu	Ala	Val	Leu	Leu	Ala	Val	Val	Phe	Met	Met	Val	
		20					25						30		
Leu	Pro	Leu	Pro	Pro	Leu	Val	Leu	Asp	Ile	Leu	Ile	Ala	Val	Asn	Met
		35						40					45		
Thr	Ile	Ser	Val	Val	Leu	Leu	Met	Ile	Ala	Ile	Tyr	Ile	Asn	Ser	Pro
		50				55					60				
Leu	Gln	Phe	Ser	Ala	Phe	Pro	Ala	Val	Leu	Leu	Val	Thr	Thr	Leu	Phe
	65				70					75				80	
Arg	Leu	Ala	Leu	Ser	Val	Ser	Thr	Thr	Arg	Met	Ile	Leu	Leu	Gln	Ala
		85						90					95		
Asp	Ala	Gly	Gln	Ile	Val	Tyr	Thr	Phe	Gly	Asn	Phe	Val	Val	Gly	Gly
		100						105					110		
Asn	Leu	Ile	Val	Gly	Ile	Val	Ile	Phe	Leu	Ile	Ile	Thr	Ile	Val	Gln
		115					120					125			
Phe	Leu	Val	Ile	Thr	Lys	Gly	Ser	Glu	Arg	Val	Ala	Glu	Val	Ser	Ala
		130			135					140					
Arg	Phe	Ser	Leu	Asp	Ala	Met	Pro	Gly	Lys	Gln	Met	Ser	Ile	Asp	Gly
	145					150				155			160		
Asp	Met	Arg	Ala	Gly	Val	Ile	Asp	Val	Asn	Glu	Ala	Arg	Glu	Arg	Arg
					165				170				175		
Ala	Thr	Ile	Glu	Lys	Glu	Ser	Gln	Met	Phe	Gly	Ser	Met	Asp	Gly	Ala
			180					185					190		

Met Lys Phe Val Lys Gly Asp Ala Ile Ala Gly Leu Ile Ile Ile Phe
195 200 205

Val Asn Ile Leu Gly Gly Val Thr Ile Gly Val Thr Gln Lys Gly Leu
210 215 220

Ala Ala Ala Glu Ala Leu Gln Leu Tyr Ser Ile Leu Thr Val Gly Asp
225 230 235 240

Gly Met Val Ser Gln Val Pro Ala Leu Leu Ile Ala Ile Thr Ala Gly
245 250 255

Ile Ile Val Thr Arg Val Ser Ser Glu Asp Ser Ser Asp Leu Gly Ser
260 265 270

Asp Ile Gly Lys Gln Val Val Ala Gln Pro Lys Ala Met Leu Ile Gly
275 280 285

Gly Val Leu Leu Leu Leu Phe Gly Leu Ile Pro Gly Phe Pro Thr Val
290 295 300

Thr Phe Leu Ile Leu Ala Leu Leu Val Gly Cys Gly Gly Tyr Met Leu
305 310 315 320

Ser Arg Lys Gln Ser Arg Asn Asp Glu Ala Asn Gln Asp Leu Gln Ser
325 330 335

Ile Leu Thr Ser Gly Ser Gly Ala Pro Ala Ala Arg Thr Lys Ala Lys
340 345 350

Thr Ser Gly Ala Asn Lys Gly Arg Leu Gly Glu Gln Glu Ala Phe Ala
355 360 365

Met Thr Val Pro Leu Leu Ile Asp Val Asp Ser Ser Gln Gln Glu Ala
370 375 380

Leu Glu Ala Asn Ala Leu Asn Asp Glu Leu Val Arg Val Arg Arg Ala
385 390 395 400

Leu Tyr Leu Asp Leu Gly Val Pro Phe Pro Gly Ile His Leu Arg Phe
405 410 415

Asn Glu Gly Met Gly Glu Gly Glu Tyr Ile Ile Ser Leu Gln Glu Val
420 425 430

Pro Val Ala Arg Gly Glu Leu Lys Ala Gly Tyr Leu Leu Val Arg Glu
435 440 445

Ser Val Ser Gln Leu Glu Leu Leu Gly Ile Pro Tyr Glu Lys Gly Glu
450 455 460

His Leu Leu Pro Asp Gln Glu Ala Phe Trp Val Ser Val Glu Tyr Glu
465 470 475 480

Glu Arg Leu Glu Lys Ser Gln Leu Glu Phe Phe Ser His Ser Gln Val
485 490 495

Leu Thr Trp His Leu Ser His Val Leu Arg Glu Tyr Ala Glu Asp Phe
500 505 510

Ile Gly Ile Gln Glu Thr Arg Tyr Leu Leu Glu Gln Met Glu Gly Gly
515 520 525

Tyr Gly Glu Leu Ile Lys Glu Val Gln Arg Ile Val Pro Leu Gln Arg
530 535 540

Met Thr Glu Ile Leu Gln Arg Leu Val Gly Glu Asp Ile Ser Ile Arg
545 550 555 560

Asn Met Arg Ser Ile Leu Glu Ala Met Val Glu Trp Gly Gln Lys Glu
565 570 575

Lys Asp Val Val Gln Leu Thr Glu Tyr Ile Arg Ser Ser Leu Lys Arg
580 585 590

Tyr Ile Cys Tyr Lys Tyr Ala Asn Gly Asn Asn Ile Leu Pro Ala Tyr
595 600 605

Leu Phe Asp Gln Glu Val Glu Glu Lys Ile Arg Ser Gly Val Arg Gln
610 615 620

Thr Ser Ala Gly Ser Tyr Leu Ala Leu Glu Pro Ala Val Thr Glu Ser
625 630 635 640

Leu Leu Glu Gln Val Arg Lys Thr Ile Gly Asp Leu Ser Gln Ile Gln
645 650 655

Ser Lys Pro Val Leu Ile Val Ser Met Asp Ile Arg Arg Tyr Val Arg
660 665 670

Lys Leu Ile Glu Ser Glu Tyr Tyr Gly Leu Pro Val Leu Ser Tyr Gln
675 680 685

Glu Leu Thr Gln Gln Ile Asn Ile Gln Pro Leu Gly Arg Ile Cys Leu
690 695 700

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Leu Leu Ser Leu Leu Asn Ser Ala Arg Leu Arg Pro Glu Leu Leu
1 5 10 15

Ile Leu Val Leu Met Val Met Ile Ile Ser Met Phe Val Ile Pro Leu
20 25 30

Pro Thr Tyr Leu Val Asp Phe Leu Ile Ala Leu Asn Ile Val Leu Ala
35 40 45

Ile Leu Val Phe Met Gly Ser Phe Tyr Ile Asp Arg Ile Leu Ser Phe
50 55 60

Ser Thr Phe Pro Ala Val Leu Leu Ile Thr Thr Leu Phe Arg Leu Ala
65 70 75 80

Leu Ser Ile Ser Thr Ser Arg Leu Ile Leu Ile Glu Ala Asp Ala Gly
85 90 95

Glu Ile Ile Ala Thr Phe Gly Gln Phe Val Ile Gly Asp Ser Leu Ala
100 105 110

Val Gly Phe Val Val Phe Ser Ile Val Thr Val Val Gln Phe Ile Val
115 120 125

Ile Thr Lys Gly Ser Glu Arg Val Ala Glu Val Ala Ala Arg Phe Ser
130 135 140

Leu Asp Gly Met Pro Gly Lys Gln Met Ser Ile Asp Ala Asp Leu Lys
145 150 155 160

Ala Gly Ile Ile Asp Ala Asp Ala Ala Arg Glu Arg Arg Ser Val Leu
165 170 175

Glu Arg Glu Ser Gln Leu Tyr Gly Ser Phe Asp Gly Ala Met Lys Phe
180 185 190

Ile Lys Gly Asp Ala Ile Ala Gly Ile Ile Ile Phe Val Asn Phe
195 200 205

Ile Gly Gly Ile Ser Val Gly Met Thr Arg His Gly Met Asp Leu Ser
210 215 220

Ser Ala Leu Ser Thr Tyr Thr Met Leu Thr Ile Gly Asp Gly Leu Val
225 230 235 240

Ala Gln Ile Pro Ala Leu Leu Ile Ala Ile Ser Ala Gly Phe Ile Val
245 250 255

Thr Arg Val Asn Gly Asp Thr Asp Asn Met Gly Arg Asn Ile Met Thr
260 265 270

Gln Leu Leu Asn Asn Pro Phe Val Leu Val Val Thr Ala Ile Leu Thr
275 280 285

Ile Ser Met Gly Thr Leu Pro Gly Phe Pro Leu Pro Val Phe Val Ile
290 295 300

Leu Ser Val Val Leu Ser Val Leu Phe Tyr Phe Lys Phe Arg Glu Ala
305 310 315 320

Lys Arg Ser Ala Ala Lys Pro Lys Thr Ser Lys Gly Glu Gln Pro Leu
325 330 335

Ser Ile Glu Glu Lys Glu Gly Ser Ser Leu Gly Leu Ile Gly Asp Leu
340 345 350

Asp Lys Val Ser Thr Glu Thr Val Pro Leu Ile Leu Val Pro Lys
355 360 365

Ser Arg Arg Glu Asp Leu Glu Lys Ala Gln Leu Ala Glu Arg Leu Arg
370 375 380

Ser Gln Phe Phe Ile Asp Tyr Gly Val Arg Leu Pro Glu Val Leu Leu
385 390 395 400

Arg Asp Gly Glu Gly Leu Asp Asp Asn Ser Ile Val Leu Leu Ile Asn
405 410 415

Glu Ile Arg Val Glu Gln Phe Thr Val Tyr Phe Asp Leu Met Arg Val
420 425 430

Val Asn Tyr Ser Asp Glu Val Val Ser Phe Gly Ile Asn Pro Thr Ile
435 440 445

His Gln Gln Gly Ser Ser Gln Tyr Phe Trp Val Thr His Glu Glu Gly
450 455 460

Glu Lys Leu Arg Glu Leu Gly Tyr Val Leu Arg Asn Ala Leu Asp Glu
465 470 475 480

Leu Tyr His Cys Leu Ala Val Thr Val Ala Arg Asn Val Asn Glu Tyr
485 490 495

Phe Gly Ile Gln Glu Thr Lys His Met Leu Asp Gln Leu Glu Ala Lys
500 505 510

Phe Pro Asp Leu Leu Lys Glu Val Leu Arg His Ala Thr Val Gln Arg
515 520 525

Ile Ser Glu Val Leu Gln Arg Leu Leu Ser Glu Arg Val Ser Val Arg
530 535 540

Asn Met Lys Leu Ile Met Glu Ala Leu Ala Leu Trp Ala Pro Arg Glu
545 550 555 560

Lys Asp Val Ile Asn Leu Val Glu His Ile Arg Gly Ala Met Ala Arg
565 570 575

Tyr Ile Cys His Lys Phe Ala Asn Gly Gly Glu Leu Arg Ala Val Met
580 585 590

Val Ser Ala Glu Val Glu Asp Val Ile Arg Lys Gly Ile Arg Gln Thr
595 600 605

Ser Gly Ser Thr Phe Leu Ser Leu Asp Pro Glu Ala Ser Ala Asn Leu
610 615 620

Met Asp Leu Ile Thr Leu Lys Leu Asp Asp Leu Leu Ile Ala His Lys
625 630 635 640

Asp Leu Val Leu Leu Thr Ser Val Asp Val Arg Arg Phe Ile Lys Lys
645 650 655

Met Ile Glu Gly Arg Phe Pro Asp Leu Glu Val Leu Ser Phe Gly Glu
660 665 670

Ile Ala Asp Ser Lys Ser Val Asn Val Ile Lys Thr Ile
675 680 685

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Val Met Ile Ile Ala Met Leu Ile Ile Pro Leu Pro Thr Tyr Leu
1 5 10 15

Val Asp Phe Leu Ile Gly Leu Asn Ile Val Leu Ala Ile Leu Val Phe
20 25 30

Met Gly Ser Phe Tyr Ile Glu Arg Ile Leu Ser Phe Ser Thr Phe Pro
35 40 45

Ser Val Leu Leu Ile Thr Thr Leu Phe Arg Leu Ala Leu Ser Ile Ser
50 55 60

Thr Ser Arg Leu Ile Leu Val Asp Ala Asp Arg Gly Lys Ile Ile Thr
65 70 75 80

Thr Phe Gly Gln Phe Val Ile Gly Asp Ser Leu Ala Val Gly Phe Val
85 90 95

Ile Phe Ser Ile Val Thr Val Val Gln Phe Ile Val Ile Thr Lys Gly
100 105 110

Ser Glu Arg Val Ala Glu Val Ala Ala Arg Phe Ser Leu Asp Gly Met
115 120 125

Pro Gly Lys Gln Met Ser Ile Asp Ala Asp Leu Lys Ala Gly Ile Ile
130 135 140

Asp Ala Ala Gly Ala Lys Glu Arg Arg Ser Ile Leu Glu Arg Glu Ser
145 150 155 160

Gln Leu Tyr Gly Ser Phe Asp Gly Ala Met Lys Phe Ile Lys Gly Asp
165 170 175

Ala Ile Ala Gly Ile Ile Ile Phe Val Asn Leu Ile Gly Gly Ile
180 185 190

Ser Val Gly Met Ser Gln His Gly Met Ser Leu Ser Gly Ala Leu Ser
195 200 205

Thr Tyr Thr Ile Leu Thr Ile Gly Asp Gly Leu Val Ser Gln Ile Pro
210 215 220

Ala Leu Leu Ile Ser Ile Ser Ala Gly Phe Met Leu Thr Arg Val Asn
225 230 235 240

Gly Asp Ser Asp Asn Met Gly Arg Asn Ile Met Ser Gln Ile Phe Gly
245 250 255

Asn Pro Phe Val Leu Ile Val Thr Ser Ala Leu Ala Leu Ala Ile Gly
260 265 270

Met Leu Pro Gly Phe Pro Phe Val Phe Phe Leu Ile Ala Val Thr
275 280 285

Leu Thr Ala Leu Phe Tyr Tyr Lys Lys Val Val Glu Lys Glu Lys Ser
290 295 300

Leu Ser Glu Ser Asp Ser Ser Gly Tyr Thr Gly Thr Phe Asp Ile Asp
305 310 315 320

Asn Thr His Asp Ser Ser Leu Ala Met Ile Glu Asn Leu Asp Arg Ile
325 330 335

Ser Ser Glu Thr Val Pro Leu Ile Leu Leu Phe Ala Glu Asn Lys Ile
340 345 350

Asn Ala Asn Asp Met Glu Gly Leu Ile Glu Arg Ile Arg Ser Gln Phe
355 360 365

Phe Ile Asp Tyr Gly Val Arg Leu Pro Thr Ile Leu Tyr Arg Thr Ser
370 375 380

Asn Glu Leu Lys Val Asp Asp Ile Val Leu Leu Ile Asn Glu Val Arg
385 390 395 400

Ala Asp Ser Phe Asn Ile Tyr Phe Asp Lys Val Cys Ile Thr Asp Glu
405 410 415

Asn Gly Asp Ile Asp Ala Leu Gly Ile Pro Val Val Ser Thr Ser Tyr
420 425 430

Asn Glu Arg Val Ile Ser Trp Val Asp Val Ser Tyr Thr Glu Asn Leu
435 440 445

Thr Asn Ile Asp Ala Lys Ile Lys Ser Ala Gln Asp Glu Phe Tyr His
450 455 460

Gln Leu Ser Gln Ala Leu Leu Asn Asn Ile Asn Glu Ile Phe Gly Ile
465 470 475 480

Gln Glu Thr Lys Asn Met Leu Asp Gln Phe Glu Asn Arg Tyr Pro Asp
485 490 495

Leu Leu Lys Glu Val Phe Arg His Val Thr Ile Gln Arg Ile Ser Glu
500 505 510

Val Leu Gln Arg Leu Leu Gly Glu Asn Ile Ser Val Arg Asn Leu Lys
515 520 525

Leu Ile Met Glu Ser Leu Ala Leu Trp Ala Pro Arg Glu Lys Asp Val
530 535 540

Ile Thr Leu Val Glu His Val Arg Ala Ser Leu Ser Arg Tyr Ile Cys
545 550 555 560

Ser Lys Ile Ala Val Ser Gly Glu Ile Lys Val Val Met Leu Ser Gly
565 570 575

Tyr Ile Glu Asp Ala Ile Arg Lys Gly Ile Arg Gln Thr Ser Gly Gly
580 585 590

Ser Phe Leu Asn Met Asp Ile Glu Val Ser Asp Glu Val Met Glu Thr
595 600 605

Leu Ala His Ala Leu Arg Glu Leu Arg Asn Ala Lys Lys Asn Phe Val
610 615 620

Leu Leu Val Ser Val Asp Ile Arg Arg Phe Val Lys Arg Leu Ile Asp
625 630 635 640

Asn Arg Phe Lys Ser Ile Leu Val Ile Ser Tyr Ala Glu Ile Asp Glu
645 650 655

Ala Tyr Thr Ile Asn Val Leu Lys Thr Ile
660 665

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cont*